```
       10                  30                  50
CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA
       70                  90                  110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC
       130                 150                 170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
         M  E  Q  R  G  Q  N  A  P  A  A  S  G  A  R  K  R
       190                 210                 230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H  G  P  G  P  R  E  A  R  G  A  R  P  G  P  R  V  P  K  T
       250                 270                 290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L  V  L  V  V  A  A  V  L  L  L  V  S  A  E  S  A  L  I  T
       310                 330                 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q  Q  D  L  A  P  Q  Q  R  A  A  P  Q  Q  K  R  S  S  P  S
       370                 390                 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E  G  L  C  P  P  G  H  H  I  S  E  D  G  R  D  C  I  S  C
       430                 450                 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K  Y  G  Q  D  Y  S  T  H  W  N  D  L  L  F  C  L  R  C  T
       490                 510                 530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R  C  D  S  G  E  V  E  L  S  P  C  T  T  T  R  N  T  V  C
       550                 570                 590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q  C  E  E  G  T  F  R  E  E  D  S  P  E  M  C  R  K  C  R
       610                 630                 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T  G  C  P  R  G  M  V  K  V  G  D  C  T  P  W  S  D  I  E
       670                 690                 710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C  V  H  K  E  S  G  I  I  I  G  V  T  V  A  A  V  V  L  I
       730                 750                 770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V  A  V  F  V  C  K  S  L  L  W  K  K  V  L  P  Y  L  K  G
       790                 810                 830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I  C  S  G  G  G  G  D  P  E  R  V  D  R  S  S  Q  R  P  G
```

FIG. 1A

```
        850                         870                         890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A  E  D  N  V  L  N  E  I  V  S  I  L  Q  P  T  Q  V  P  E
        910                         930                         950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q  E  M  E  V  Q  E  P  A  E  P  T  G  V  N  M  L  S  P  G
        970                         990                        1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E  S  E  H  L  L  E  P  A  E  A  E  R  S  Q  R  R  R  L  L
       1030                        1050                        1070
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V  P  A  N  E  G  D  P  T  E  T  L  R  Q  C  F  D  D  F  A
       1090                        1110                        1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D  L  V  P  F  D  S  W  E  P  L  M  R  K  L  G  L  M  D  N
       1150                        1170                        1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E  I  K  V  A  K  A  E  A  A  G  H  R  D  T  L  Y  T  M  L
       1210                        1230                        1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I  K  W  V  N  K  T  G  R  D  A  S  V  H  T  L  L  D  A  L
       1270                        1290                        1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E  T  L  G  E  R  L  A  K  Q  K  I  E  D  H  L  L  S  S  G
       1330                        1350                        1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K  F  M  Y  L  E  G  N  A  D  S  A  M  S  *
       1390                        1410                        1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
       1450                        1470                        1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
       1510                        1530                        1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC
       1570                        1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA
```

FIG.1B

```
1   M - L G - - - - - - - - - - - - - - - - - - - - - - - - - - - I W T L L P L V L   h Fas protein
1   M G L S - - - - - - - - - - - - - - - - - - - - - - - - - - - T V P D L L L P L   h TNFR I Protein
1   M E Q R - - - - - - - - - - - - - - - - - - - - - - - - - - - P R G C A A V A A   DR3 protein
1   M E Q R G Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L   HLYBX88XXprotein

13  T S V A R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L   h Fas protein
14  V L L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G K Y I H - -   h TNFR I Protein
14  A L L L V L L G A R A Q G - - - - - - - - G T R S P R - C D C A - G D F - H - -   DR3 protein
41  V V A A V L L L V S A E S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L   HLYBX88XXprotein

53  H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E Y T   h Fas protein
52  P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A   h TNFR I Protein
41  K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A   DR3 protein
81  - - - - - - - - - - C P P G H H I S E D - - - - - - G R D C I S C K Y G Q D Y S   HLYBX88XXprotein

93  D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N   h Fas protein
92  S E N H L R - H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N   h TNFR I Protein
81  W E N H H N S E C A R C Q A C D E Q A S Q V A L E N C S A V A D T R C G C K P G   DR3 protein
105 T H W N D L L F C L R C T R C D - - S G E V E L S P C T T T R N T V C Q C E E G   HLYBX88XXprotein

133 F F - - - - - - - - - - C N S T V - - - C E H C D P C T K - - - - - - - - - - -   h Fas protein
131 Q Y R H Y W S E N L F Q C - - - - - F N C S L C L N - G T V H - - - - L S C Q E   h TNFR I Protein
121 W F V E C - - - Q V S Q C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R   DR3 protein
143 T F R E - - - - - - - - - - E D S P E M C R K C - - - - - - - - - - R T G C P R   HLYBX88XXprotein
```

FIG.2A

```
149 - - - - - - - C E H G I I - - - K E C - - - - - - - - T L T S N T K C K E - - -   h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P Q I E   h TNFR I Protein
158 R D T D C G T C L P G F Y E H G D G C V S C P T S T L G - S C P E R C A A V C G   DR3 protein
163 G M V K V G D C T P - - - W S D I E C V - - - - - - - - - - - H K E S G I I I G   HLYBX88XXprotein

168 - - - - - E G S R S N L G W - - - - - - - L C L L - L L P I P L I V - - - - - W   h Fas protein
201 N V K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W   h TNFR I Protein
197 W R Q - - - - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W   DR3 protein
189 - - - - - - V T V A A V V L I V A V F - - V C K S L L W K K V L P Y L K G I C S   HLYBX88XXprotein

190 V K R K E V Q K T C R K H R K E N Q G S H E S - - - - - - - - - - - - - - - - -   h Fas protein
240 - K S K L Y S I V C G K S T P E K E G E L E G T T T K P L A P N P S F S P T P G   h TNFR I Protein
229 - P H K P L - V T A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D   DR3 protein
221 - - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q   HLYBX88XXprotein

213 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   h Fas protein
279 F T P T L G F S P V P S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P   h TNFR I Protein
267 S S E K I C T V Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - - P   DR3 protein
255 V P E Q E M E V Q E P A E - - - - - - P T G V N M L S P G - - - E S E H L - - -   HLYBX88XXprotein

213 - - - - - - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M   h Fas protein
318 Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A   h TNFR I Protein
305 S R A L G P A A A P T L S P - - - - - - - - - - E S P A G S P A M M L Q P G P Q   DR3 protein
283 - - - - - - - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q   HLYBX88XXprotein
```

FIG.2B

```
241 TLSQV---------KGFVRKNGVNEAKIDEIKNDNVQDTA h Fas protein
358 TLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLR h TNFR I Protein
335 -LYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FR DR3 protein
312 CFDDFADLVPFDSWEPLMRKLGLMDNEI-KVAKAEAAGHR HLYBX88XXprotein

272 EQKVQLLRNWHQLHGKKEA-YDTLIKDLKKANLCTLAEKI h Fas protein
398 EAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDI h TNFR I Protein
373 DQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL DR3 protein
351 DTLYTMLIKWVNKTGR-DASVHTLLDALETLGERLAKQKI HLYBX88XXprotein

311 QTIILKDITSDSENSNFRNEIQSLV                h Fas protein
438 EEAL-------CGPAALPPAPSLLR                h TNFR I Protein
410 -------------RSRLQRGP                    DR3 protein
390 EDHLLSSGKFMYLEGN--ADSAMS                 HLYBX88XXprotein
```

FIG.2C

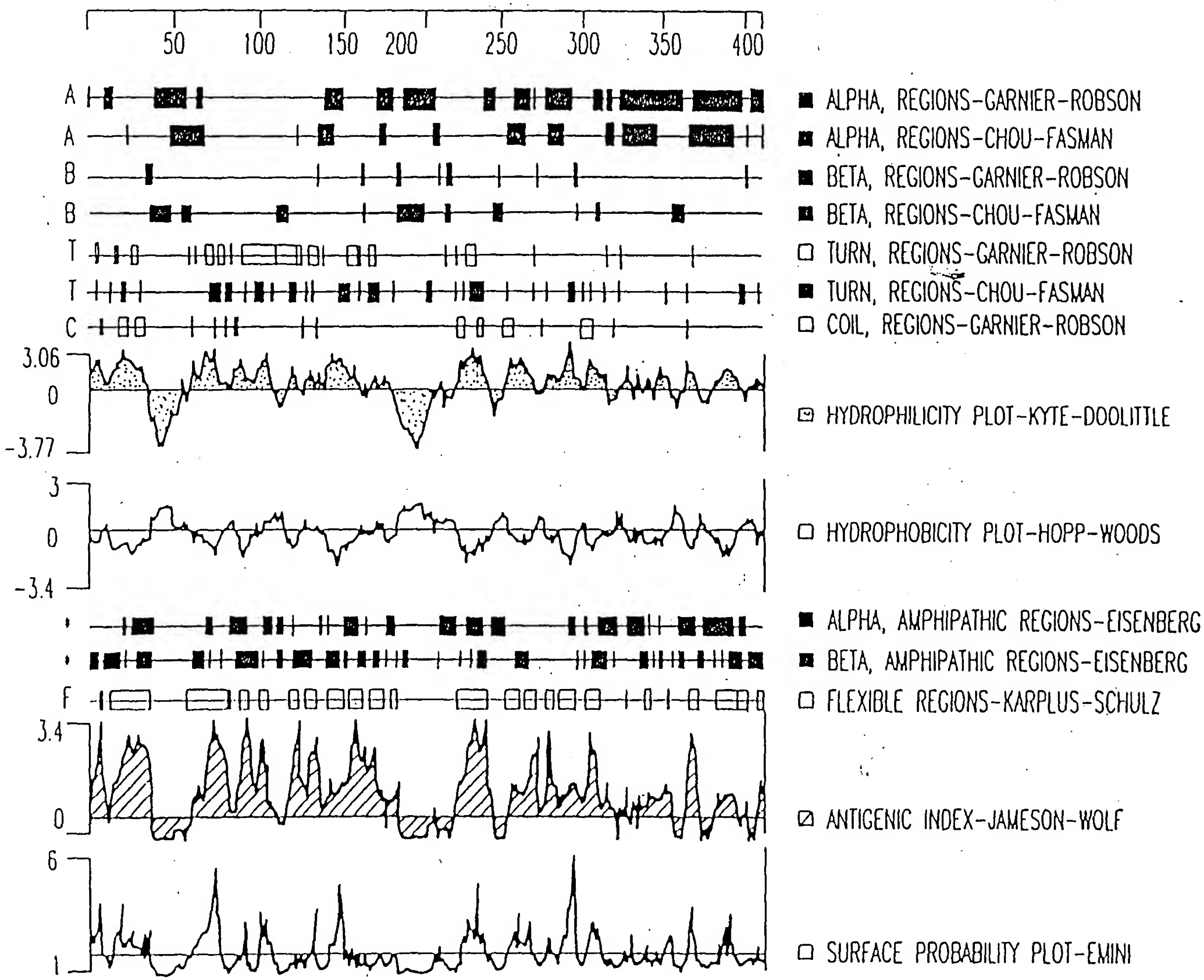

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
3.06
0
-3.77
3
0
-3.4
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.3

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
```

FIG.4

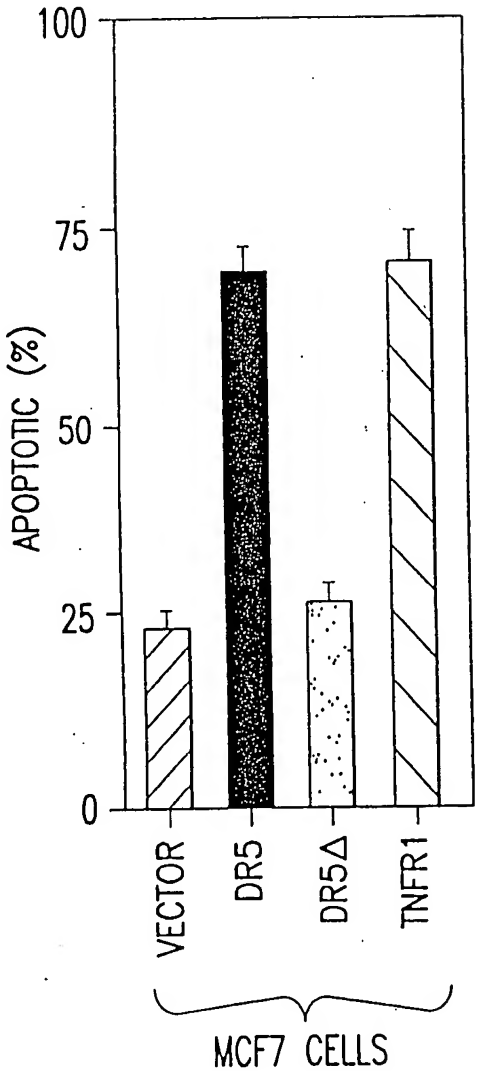


FIG. 5A

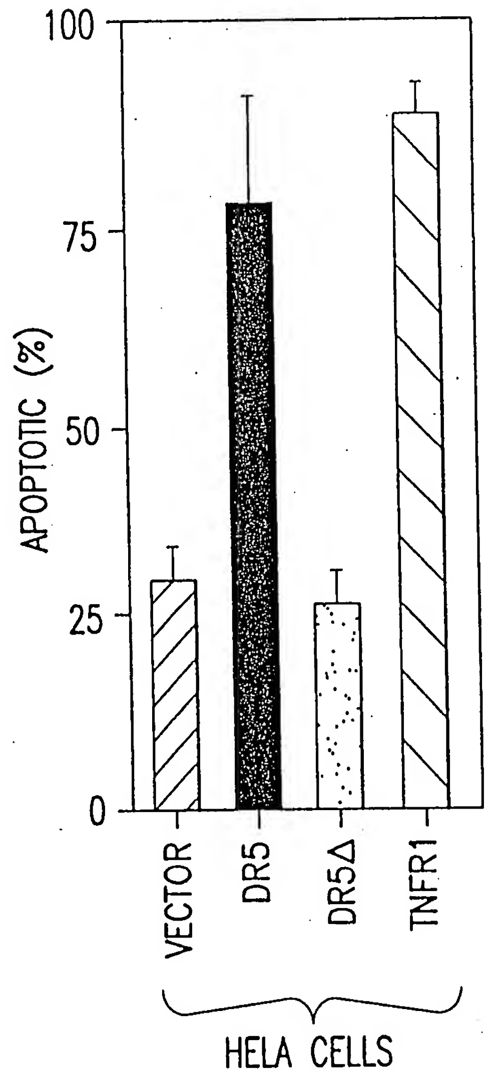


FIG. 5B

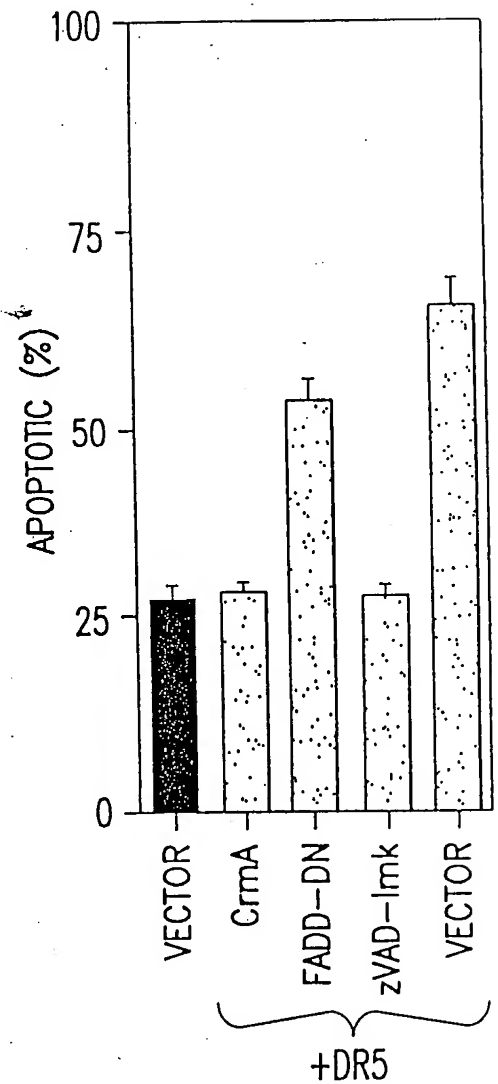


FIG. 5C

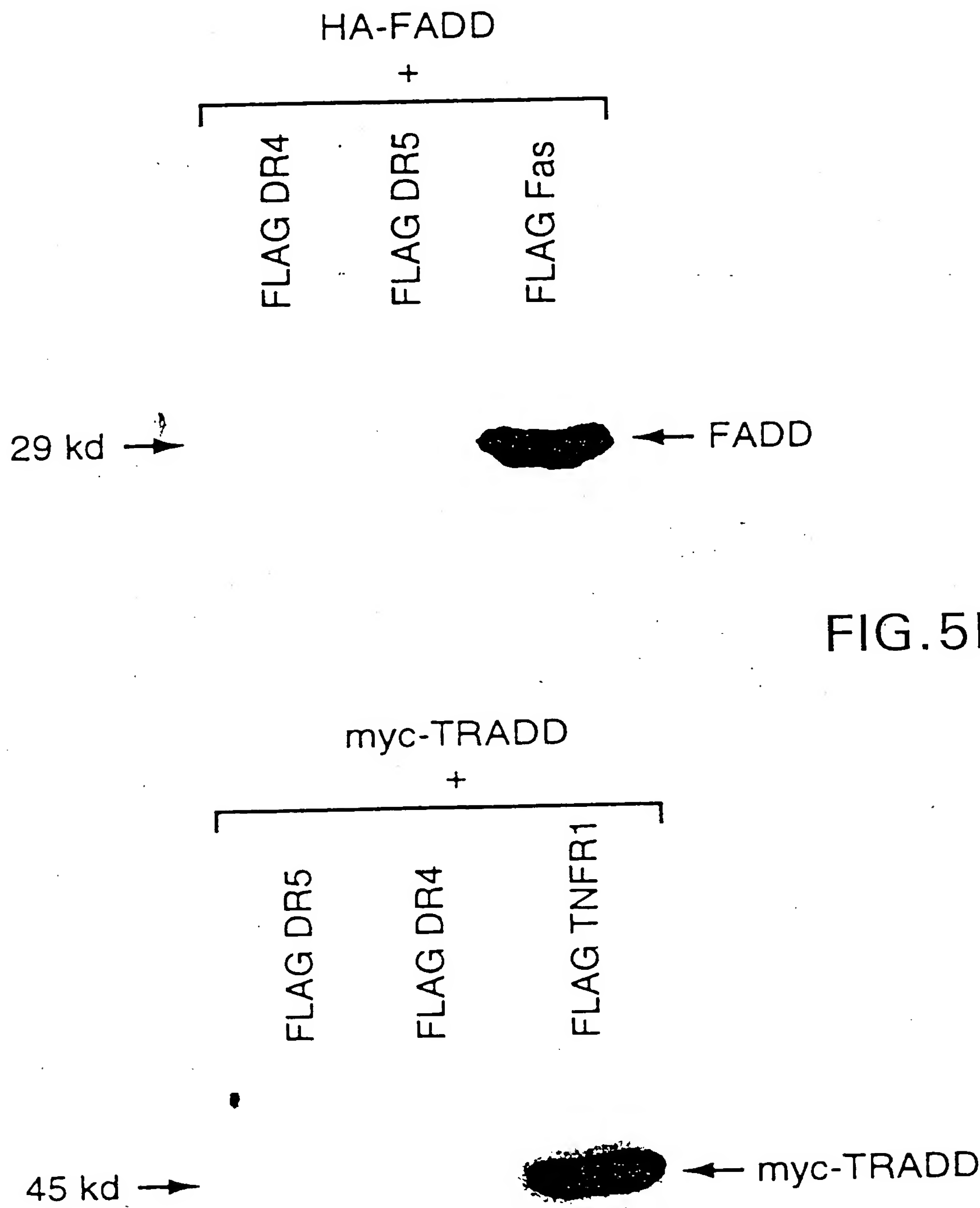
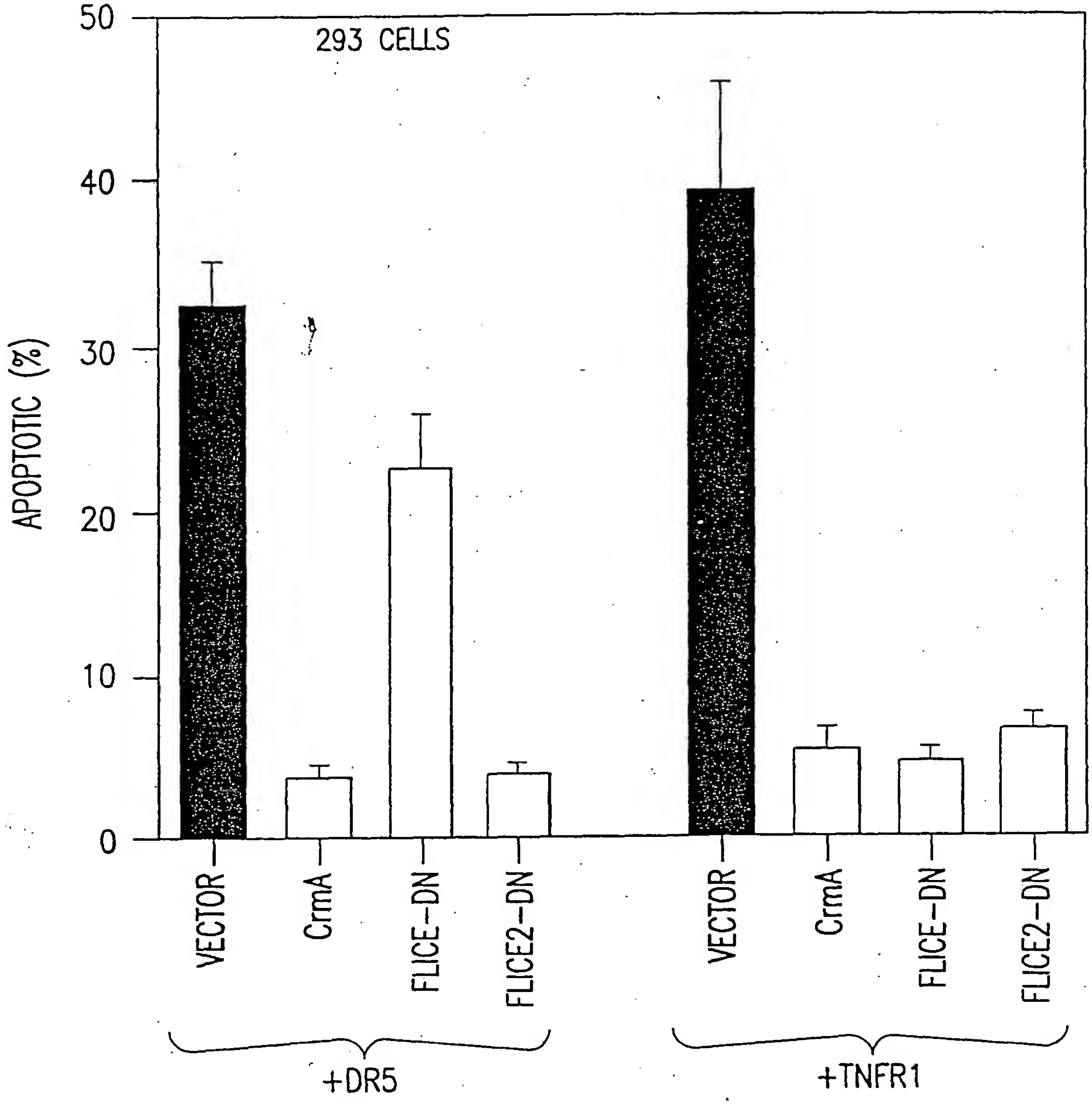

HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD
myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD

FIG.5D



293 CELLS
APOPTOTIC (%)
50
40
30
20
10
0
VECTOR
CrmA
FLICE-DN
FLICE2-DN
VECTOR
CrmA
FLICE-DN
FLICE2-DN
+DR5
+TNFR1

FIG. 5E

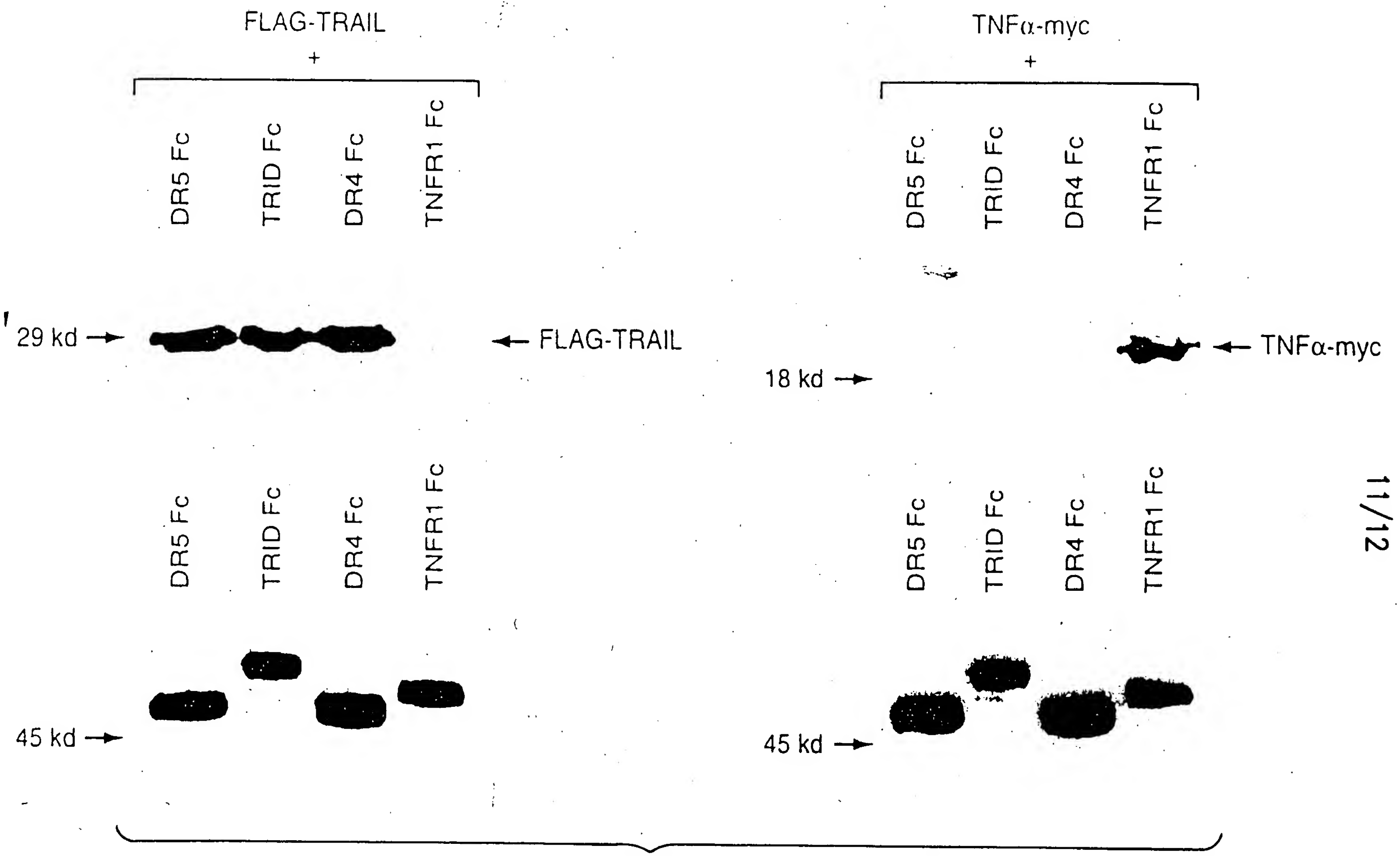

FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
45 kd
TNFα-myc
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
18 kd
TNFα-myc
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
45 kd

FIG.6A

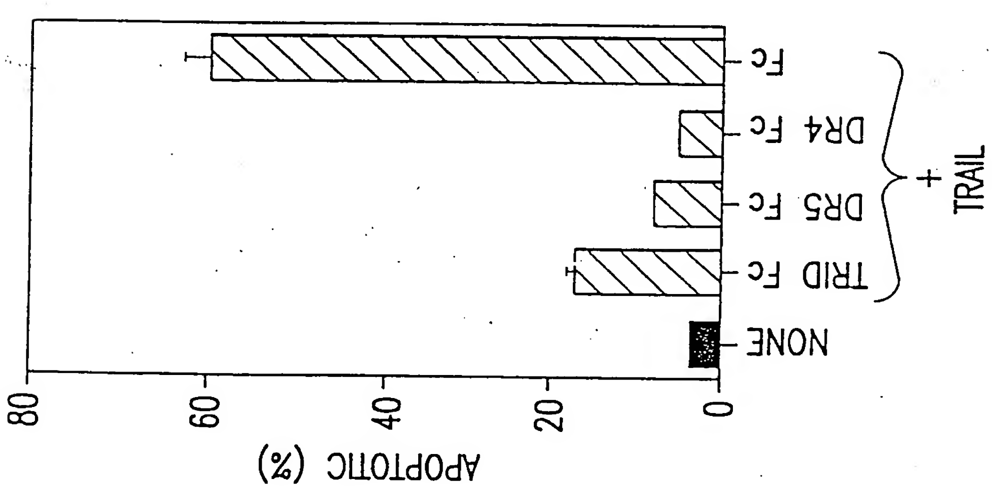

APOPTOTIC (%)
0
20
40
60
80
NONE
TRID Fc
DR5 Fc
DR4 Fc
Fc
+ TRAIL

FIG. 6B

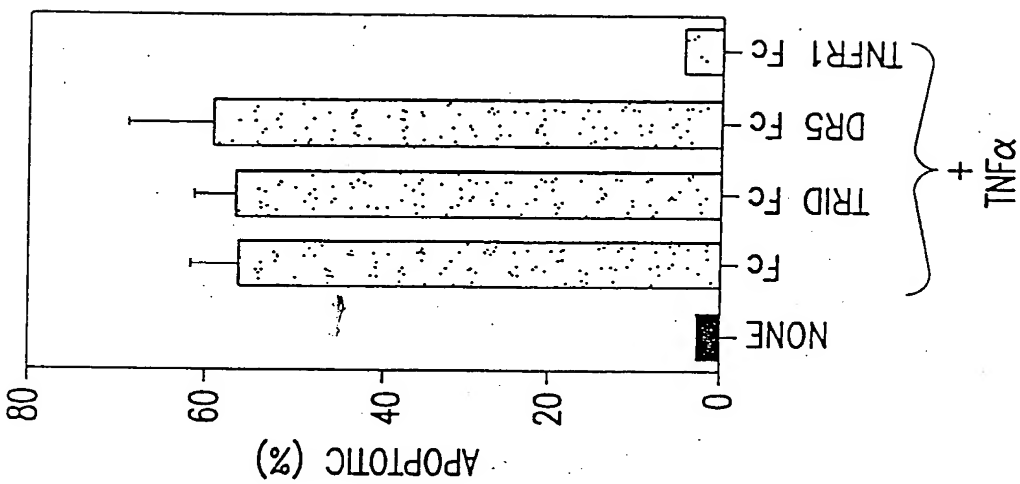

APOPTOTIC (%)
0
20
40
60
80
NONE
Fc
TRID Fc
DR5 Fc
TNFR1 Fc
+ TNFα

FIG. 6C